

1	ACCAGACAGAGGACTCTCATTAAGGAAG	TGCTCTGTGCTGACCCCTACAAGATGCCA	AGAGAAGATGCTCATTCTATCTATGTTTAC	CCCAAGAGGGGCGACGGCCACTCTTACACC	119
120	ACGGCTAAGAGGCCCTCGGATCGGCATC	CTGACAGTGTATCTGGGAGTCTTACTGCTC	ATCGGCTGTTGGTATTGTAGACAGCAAAAT	GGATACAGAGCCCTTGCATGATTAAGTCTTT	22
23	ThrAlaGluGluAlaAlaGluVilIleGlyIla	LeuThrValIleAlaGluGlyValIleLeuLeuLeu	IleGlyCysAlaIleTyrCysAlaArgArgAen	GlyTyrArgAlaLeuMetAspLysSerLeu	239
240	CATGTTGGCACTCAATGTGCTTAAACAAG	AGATGCCCAACAAGAGGTTTGCATCATCGG	GACAGCAAGTGTCTCTTCAAGAGAGAAAAC	TGTGAACCTGTGGTTTCCCAATGCTCCACCT	62
63	HlaValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGlyPheAlaPheArg	AspSerLysValSerLeuGlnGluLysAen	CysGluProValValProAenAlaProPro	359
360	GCTTATGAGAAACTCTCTGCAAGACAGTCA	CCACGACCTTATTTCACCTTAAGAGCCAGCG	AGACACCTGACAGATGCTGAAATTTATTTCT	CTCACACTTTTGTCTTGTATTTAATACAGAC	102
103	AlaTyrGluLysLeuSerAlaGluGlnSer	ProProProTyrIleSerPro			479
480	ATCTAATGTTCTCTTTGGAAATGGGTAGG	AAATGCAAGCCATCTCTAATAATAGTC	AGTGTAAATTTTAGTAGGTCCGCTAGCA	GTAATAATCATGTGAGGAAATGATGAGAAA	118
600	TATTAAATTTGGGAAACTCCCATCAATAAAT	GTGCAATGCATGATTAATCTGTGCCAGA	GGTAAATGTTAGTAAATCCATGCTGTATT	TCTGAGACACAGAAATTCAGTGGGTATTCT	599
720	GGGGCCATCCAAATTTCTTTTACTTGAAT	TTGGCTAATACAACTAGTCAGGTTTTCG	AACCTTGACCAATGAACTGTACACAGAA	TTGTTCCAGTACTATGAGTGTCTCACAAAG	719
840	GATACTTTTACAGGTTAAGACAAAGGGTTG	ACTGGCTTATTATCTGATCAGACATGT	CAGCAATGTTCTTTGTGCTCTAATAATTTCT	ATTATACATAATATATATTTGTAAGATC	839
960	CTATAGTCTTTTTTTTTGAGATGGAGTTT	CGCTTTTGTGCTGCAAGCTGGAGTCAATG	GGCAATCTTGGCTCACCATTAACCTCCGCC	TCCCAGGTTCAAGCAATTCCTCCCTTAG	959
1080	CCTCCGAGTGTAGCTGGGATTACAGCGTGC	GCACATATGCTGACTAATTTTGTAGTTT	AGTAGAGCGGCTGAGCCACCGCTGGCT	GGCTGGTCTCAAACTGCTGACCTCAGGTGA	1079
1200	TCTGCCCGCTCAGCTCCCAAGTCTCTGG	AATTACAGCGCTGAGCCACCGCTGGCT	GGATCTATATCTTAGGTAAGACATATAAC	GCAGTCTAAATTACATTTTCTCAAGGCTC	1199
1320	AATGCTATTCTTAACTAATGACAAATTTT	CTACTAAACCAAGAAATTTGTAAGAGATT	AAATAAATAAAGCTACTATGTACTGCTCT	AGTCTGNTGCTGTGTACTGCTTAAATG	1319
1440	TACCTATGGCAATTTAGCTCTCTTGGGTTT	CCAAATCCCTCTCTCACAAGAAATGTGCAAG	AAATCATAAAGGATCAGAGATTTCTGAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	143
					1559

FIGURE 1

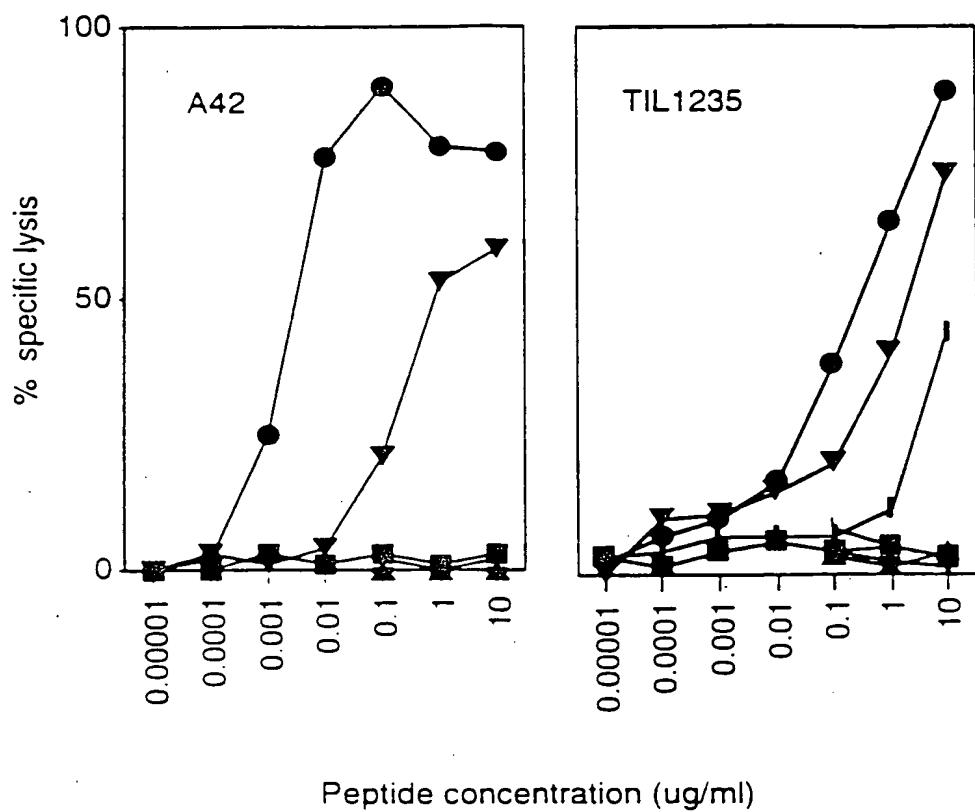


FIGURE 2

FIGURE 3A

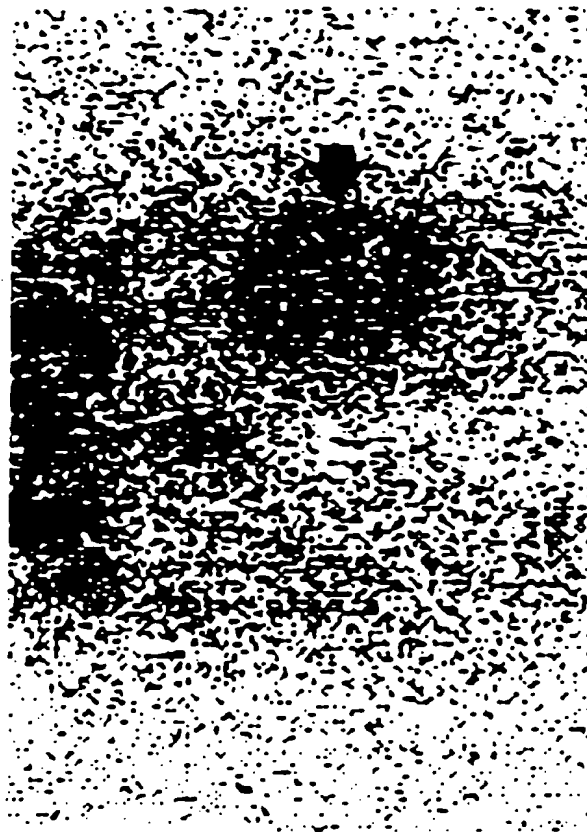
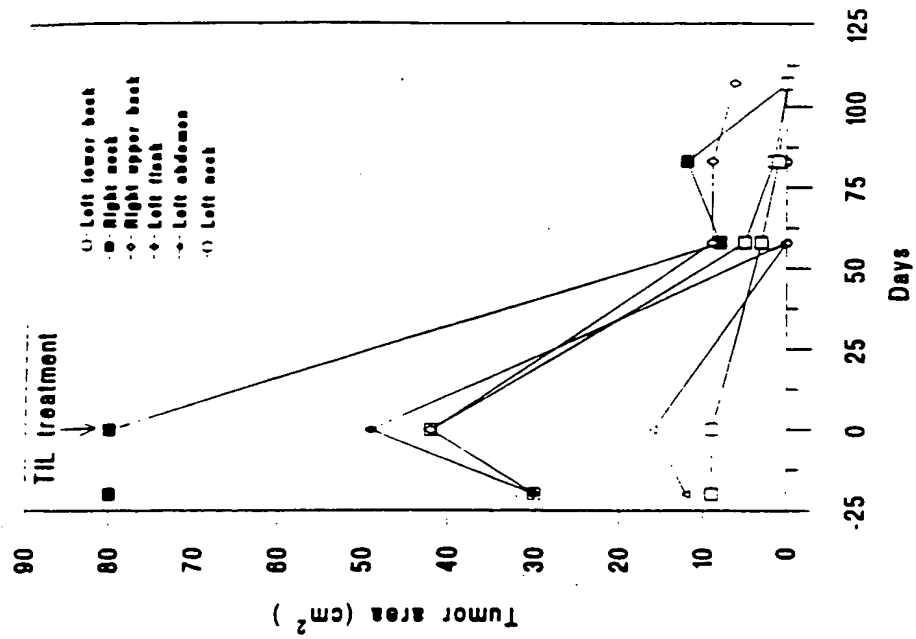


FIGURE 3B



GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
CCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGA CTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIGURE 4

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	116 C
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	120 C
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	124 C
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	128 C
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	132 C
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	136 O
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	140 O
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	144 O
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	148 O
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	152 O
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	156 O
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	160 O
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	164 O
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	168 O
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	172 O
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	176 O
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	180 O
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	184 O
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	188 O
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	192 O
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	196 O
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	200 O
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	204 O
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	208 O
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	212 O
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	216 O
AAAAAAAAAA AA	2172

FIGURE 4 (continued)

FIGURE 5A

```

1 MDLVLRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRLR TKAWNRLYP
51 EWTEAQRDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNOPLTF ALQLHDPSGY
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVPGTT DGHRTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGS LGP LLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAORL CQVLPSPAC
551 QLV LHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGOVPLIV
601 GILLVLMVV LASLIYRRRL MKQDFSVPOL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

```

FIGURE 5B

```

Pme117 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----
gp100 M-----V-----Q-----L-----
cDNA25FL M-----F-----Q-----L-----
cDNA25TR Q-----L-----PPQWAAGLSTLI
1 162 236 274 588 649

```

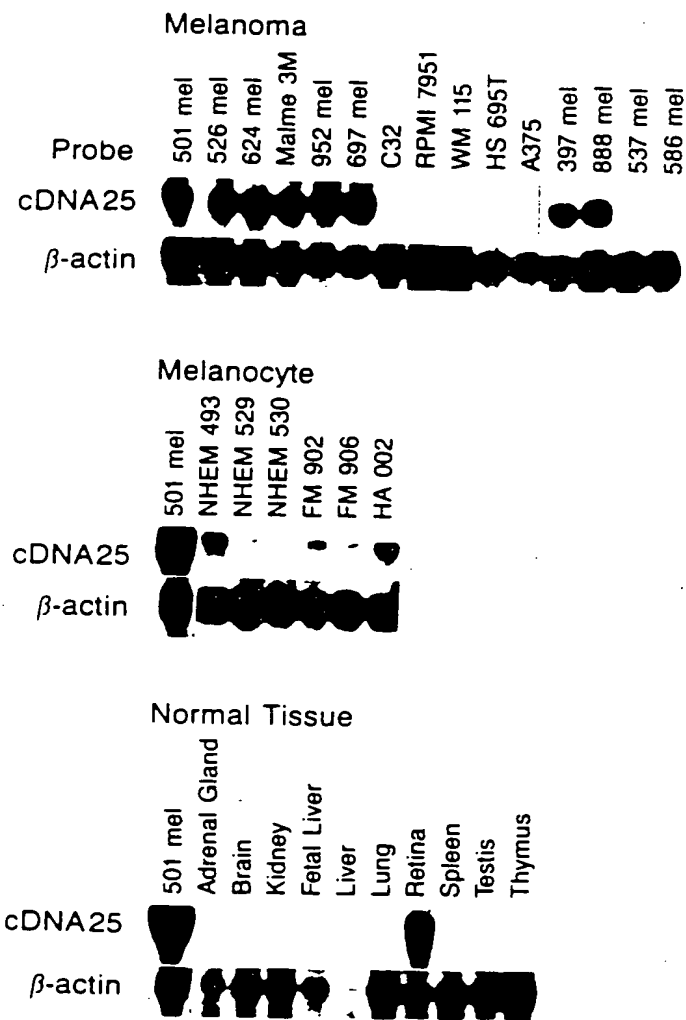


FIGURE 6